

SEQUENCE LISTING

<110> David Michalovich
Matthew Alan Sims
Narjis Shaikh

<120> NOVEL COMPOUNDS

<130> GP-30088-D1

<140> TO BE ASSIGNED
<141>

<150> US 09/184,001
<151> 1998-11-02

<150> UK 9806221.9
<151> 1998-03-23

<150> UK 9817479.0
<151> 1998-08-11

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 2186
<212> DNA
<213> HOMO SAPIENS

<400> 1

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ccgcgcctg	ccgcgggggc	cgctcggtc	ctccatggag	gccggagagg	aaccgctgct	120
gctggccgaa	ctcaagcccc	ggcgccccca	ccagtttgat	tggaaagtcca	gctgtgaaac	180
ctggagcgtc	gccttctccc	catatggctc	ctggtttgct	tggctcaag	gacactgcat	240
cgtcaaactg	atccccctggc	cgttggagga	gcagttcatc	cctaaagggt	ttgaagccaa	300
aagcgaagt	agaaaaaatg	agacgaaaagg	gcggggcagc	ccaaaagaga	agacgctgga	360
ctgtgttcag	attgtctggg	ggctggcctt	cagccctgtgg	ccttccccac	ccagcaggaa	420
gctctgggca	cgccaccacc	cccaagtgc	cgatgtctct	tgctctggttc	ttgctacggg	480
actcaacgtat	gggcagatca	agatctggg	ggtgcagaca	gggctcctgc	ttttgaatct	540
ttccggccac	caagatgtcg	tgagagatct	gagttcaca	cccagtggca	gtttgatttt	600
ggtctccgcg	tcacgggata	agactcttcg	catctgggac	ctgaataaaac	acggtaaaca	660
gattcaagtgt	ttatcgggccc	acctgcagtgc	gttttactgc	tgttccatct	ccccagactg	720
cagcatgctg	tgctctgc	ctggagagaa	gtcggtcttt	ctatggagca	tgagggtcc	780
cacgttaatt	cggaagctag	aggccatca	aagcagtgtt	gtctcttgc	acttctcccc	840
cgactctgcc	ctgcttgtca	cggcttctta	cgataccat	gtgattatgt	gggaccctta	900
cacccggcga	aggctgaggt	cactccacca	cacccaggtt	gaccccgcta	tggatgacag	960
tgacgtccac	attagctcac	tgagatctgt	gtgcttc	ccagaaggct	tgtaccttgc	1020
cacgggtggca	gatgacagac	tcctcaggat	ctggggccctg	gaactgaaaa	ctcccaattgc	1080
atttgctcct	atgaccaatg	ggcttgctg	cacattttt	ccacatggtg	gagtcatgc	1140
cacagggaca	agagatggcc	acgtccagtt	ctggacagct	ccttagggtcc	tgtcctca	1200
gaagcactta	tgccggaaag	cccttcgaag	tttcctaaaca	acttaccaag	tcctagca	1260
gccaatcccc	aagaaaaatga	aagagttcct	cacatacagg	acttttaag	caacaccaca	1320
tcttgtgctt	ctttgttagca	gggtaaatcg	tcctgtcaaa	gggagttgct	ggaataatgg	1380

<210> 2
<211> 404
<212> PRT
<213> HOMO SAPIENS

Ser Asp Val His Ile Ser Ser Leu Arg Ser Val Cys Phe Ser Pro Glu
 290 295 300
 Gly Leu Tyr Leu Ala Thr Val Ala Asp Asp Arg Leu Leu Arg Ile Trp
 305 310 315 320
 Ala Leu Glu Leu Lys Thr Pro Ile Ala Phe Ala Pro Met Thr Asn Gly
 325 330 335
 Leu Cys Cys Thr Phe Phe Pro His Gly Gly Val Ile Ala Thr Gly Thr
 340 345 350
 Arg Asp Gly His Val Gln Phe Trp Thr Ala Pro Arg Val Leu Ser Ser
 355 360 365
 Leu Lys His Leu Cys Arg Lys Ala Leu Arg Ser Phe Leu Thr Thr Tyr
 370 375 380
 Gln Val Leu Ala Leu Pro Ile Pro Lys Lys Met Lys Glu Phe Leu Thr
 385 390 395 400
 Tyr Arg Thr Phe

<210> 3
 <211> 2558
 <212> DNA
 <213> HOMO SAPIENS
 <220> FEATURE
 <221> UNSURE
 <222> (146) (161) (178) (233) (254) (296)
 <223> OTHER INFORMATION: Partial DNA sequence derived from EST sequences.

<400> 3

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ctcaaggaca	ctgcatcg	aaactnatcc	cctggccgtt	ngaggagcag	ttcatccnta	180
aagggttta	agccaaaagc	cgaagtagca	aaaatgagac	gaaaggcgg	gnagnatccaa	240
aagagaagac	gctngactgt	ggtcagattt	tctggggct	ggccttcagc	ctgtgnctt	300
ccccacccag	caggaagotc	tggcacgccc	accacccca	agtgcggat	gtctcttgcc	360
tggttcttgc	tacgggactc	cacgatggc	agatcaagat	ctgggaggt	cagacaggc	420
tcctgctttt	aatctttcc	ggccaccaag	atgtcgtag	agatctgagc	ttcacaccca	480
gtggcagttt	gattttggtc	tcccggtcac	gggataagac	tcttcgcac	tgggacactga	540
ataaacacgg	taaacagatt	caagtgttat	cgggccacct	gcagtgggtt	tactgctgtt	600
ccatctcccc	agactgcagc	atgctgtgt	ctgcagctgg	agagaagtcg	gtctttctat	660
ggagcatgag	gtcctacacg	ttaattcgg	agctagaggg	ccatcaaagc	agtgttgtct	720
cttgcactt	ctccccccgac	tctgcccgtc	ttgtcacggc	ttcttacgt	accaatgtga	780
ttatgtggaa	cccctacacc	ggcgaaaaggc	tgaggtca	ccaccacacc	cagggtgacc	840
ccgcatgg	tgacagtgac	gtccacatta	gctcaactgag	atctgtgtc	ttctctccag	900
aaggcttgc	ccttgcac	gtggcagatg	acagactct	caggatctgg	gccctggAAC	960
tgaaaactcc	cattgcattt	gctccatgt	ccaatggct	ttgtgcaca	ttttttccac	1020
atgggtggat	cattgccaca	gggacaagag	atggccacgt	ccagttctgg	acagctctta	1080
gggtcctgtc	ctcactgaag	cacttatgcc	ggaaagccct	tcgaagttt	ctaacaactt	1140
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gtgaatagaa	tgttagaaaa	ccagattcca	gtgtactagt	catggatctt	tctctccctg	1380
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taaatttca	gtccagttat	gaacagcaag	tgttgactc	tttctgttt	ttttgattca	1500
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cttcgatgtt	ggccaagttgc	ttttcttctt	gggctccctt	ctgacctgca	ggacagttt	1740
cctggagcca	tttggtatga	ggtattaaatt	tagcttaact	aaattacagg	ggactcagag	1800

gccgtgctcc	tgaccgatcc	agacactatt	actggctttt	ttttttttt	tttaacaatg	1860
gtgtgcgt	gcaggaaatg	acaatttgt	atgtcagatt	atacaaggat	gtattctaa	1920
accgcgtac	tattcagatg	gctactgagt	tatcagtggc	catttattag	catcatattt	1980
atttgtat	tctcaacaga	tgttaaggta	caactgtgtt	tttctcgatt	atctaaaaac	2040
catagtactt	aaattgaaca	gttgc当地	tgtcttaatt	gtgtaaagaa	ttgggtgttagt	2100
catgacttta	gctgatactc	ttatgtacga	gatctgtctc	tgctgtttaa	cttcatttgg	2160
ttaatcagct	ggtttcaact	ctactgc当地	acaaaaatag	ctccctaaaa	gtactgttct	2220
ccttcagtg	catgttagta	tctaatacag	acacctcatt	caaacaaaac	ctgcctttagg	2280
aaaatattaat	atattttaaa	ttatattttaaa	agaaatacaa	catcttattc	tttagcttc	2340
ttaatcgg	ctttatggag	gccagtgtaa	cgttacatga	ctcggtgaga	aagttgagga	2400
atttcctcta	ccaccttgt	tgcttgaaga	aaaacatgtc	ttttcaaat	gagaggctt	2460
cattgaagaa	aagaaaaaaaaa	caacagttaa	aagctattgg	ctctctgttt	catttttttc	2520
cattaagaaa	aaaaaaaaagtc	ccctttaaa	acaaggcag			2558

<210> 4
 <211> 400
 <212> PRT
 <213> HOMO SAPIENS
 <220> FEATURE
 <221> UNSURE
 <222> (53) (59) (98)
 <223> OTHER INFORMATION: Partial DNA sequence derived from EST sequences.

Lys	Glu	Pro	Leu	Leu	Leu	Ala	Glu	Leu	Lys	Pro	Gly	Arg	Pro	His	Gln
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Phe	Asp	Trp	Lys	Ser	Ser	Cys	Glu	Thr	Trp	Ser	Val	Ala	Phe	Ser	Pro
			20					25				30			
Asp	Gly	Ser	Trp	Phe	Ala	Trp	Ser	Gln	Gly	His	Cys	Ile	Val	Lys	Leu
			35					40			45				
Ile	Pro	Trp	Pro	Xaa	Glu	Glu	Gln	Phe	Ile	Xaa	Lys	Gly	Phe	Glu	Ala
	50				55					60					
Lys	Ser	Arg	Ser	Ser	Lys	Asn	Glu	Thr	Lys	Gly	Arg	Gly	Ser	Pro	Lys
	65				70				75			80			
Glu	Lys	Thr	Leu	Asp	Cys	Gly	Gln	Ile	Val	Trp	Gly	Leu	Ala	Phe	Ser
			85					90			95				
Leu	Xaa	Leu	Ser	Pro	Pro	Ser	Arg	Lys	Leu	Trp	Ala	Arg	His	His	Pro
			100					105			110				
Gln	Val	Pro	Asp	Val	Ser	Cys	Leu	Val	Leu	Ala	Thr	Gly	Leu	His	Asp
	115						120				125				
Gly	Gln	Ile	Lys	Ile	Trp	Glu	Val	Gln	Thr	Gly	Leu	Leu	Leu	Asn	
	130					135				140					
Leu	Ser	Gly	His	Gln	Asp	Val	Val	Arg	Asp	Leu	Ser	Phe	Thr	Pro	Ser
	145					150			155			160			
Gly	Ser	Leu	Ile	Leu	Val	Ser	Ala	Ser	Arg	Asp	Lys	Thr	Leu	Arg	Ile
			165					170			175				
Trp	Asp	Leu	Asn	Lys	His	Gly	Lys	Gln	Ile	Gln	Val	Leu	Ser	Gly	His
			180					185			190				
Leu	Gln	Trp	Val	Tyr	Cys	Cys	Ser	Ile	Ser	Pro	Asp	Cys	Ser	Met	Leu
	195						200				205				
Cys	Ser	Ala	Ala	Gly	Glu	Lys	Ser	Val	Phe	Leu	Trp	Ser	Met	Arg	Ser
	210				215				220						
Tyr	Thr	Leu	Ile	Arg	Lys	Leu	Glu	Gly	His	Gln	Ser	Ser	Val	Val	Ser
	225				230				235			240			
Cys	Asp	Phe	Ser	Pro	Asp	Ser	Ala	Leu	Leu	Val	Thr	Ala	Ser	Tyr	Asp
					245				250			255			
Thr	Asn	Val	Ile	Met	Trp	Asp	Pro	Tyr	Thr	Gly	Glu	Arg	Leu	Arg	Ser

	260		265		270
Leu His His Thr Gln Val Asp Pro Ala Met Asp Asp Ser Asp Val His					
275		280		285	
Ile Ser Ser Leu Arg Ser Val Cys Phe Ser Pro Glu Gly Leu Tyr Leu					
290		295		300	
Ala Thr Val Ala Asp Asp Arg Leu Leu Arg Ile Trp Ala Leu Glu Leu					
305		310		315	
Lys Thr Pro Ile Ala Phe Ala Pro Met Thr Asn Gly Leu Cys Cys Thr					
325		330		335	
Phe Phe Pro His Gly Gly Val Ile Ala Thr Gly Thr Arg Asp Gly His					
340		345		350	
Val Gln Phe Trp Thr Ala Pro Arg Val Leu Ser Ser Leu Lys His Leu					
355		360		365	
Cys Arg Lys Ala Leu Arg Ser Phe Leu Thr Thr Tyr Gln Val Leu Ala					
370		375		380	
Leu Pro Ile Pro Lys Lys Met Lys Glu Phe Leu Thr Tyr Arg Thr Phe					
385		390		395	